Plant breeding in the 21st century: Molecular breeding and high throughput phenotyping

Mark E. Sorrells*

Plant Breeding & Genetics Section, Cornell University, Ithaca, NY 14853 USA

Abstract

The discipline of plant breeding is experiencing a renaissance impacting crop improvement as a result of new technologies, however fundamental questions remain for predicting the phenotype and how the environment and genetics shape it. Inexpensive DNA sequencing, genotyping, new statistical methods, high throughput phenotyping and gene-editing are revolutionizing breeding methods and strategies for improving both quantitative and qualitative traits. Genomic selection (GS) models use genome-wide markers to predict performance for both phenotyped and non-phenotyped individuals. Aerial and ground imaging systems generate data on correlated traits such as canopy temperature and normalized difference vegetative index that can be combined with genotypes in multivariate models to further increase prediction accuracy and reduce the cost of advanced trials with limited replication in time and space. Design of a GS training population is crucial to the accuracy of prediction models and can be affected by many factors including population structure and composition. Prediction models can incorporate performance over multiple environments and assess GxE effects to identify a highly predictive subset of environments. We have developed a methodology for analyzing unbalanced datasets using genome-wide marker effects to group environments and identify outlier environments. Environmental covariates can be identified using a crop model and used in a GS model to predict GxE in unobserved environments and to predict performance in climate change scenarios. These new tools and knowledge challenge the plant breeder to ask the right questions and choose the tools that are appropriate for their crop and target traits. Contemporary plant breeding requires teams of people with expertise in genetics, phenotyping and statistics to improve efficiency and increase prediction accuracy in terms of genotypes, experimental design and environment sampling.

Keywords: plant breeding methods, genomic selection, high throughput phenotyping, genotype by environment interaction.

Corresponding author*Mark E. Sorrells
240 Emerson Hall
Cornell University
Ithaca, NY 14853
Ph. 607-255-1665
Fax 607-255-6683
Email: mes12@cornell.edu